ELSEVIER

Discrete Applied Mathematics 88 (1998) 397–398

DISCRETE APPLIED MATHEMATICS

Author Index

Volume 88 (1998)

Annexstein, F. and R. Swaminathan, On testing consecutive-ones property in parallel (1–3) 7– 28
Armen, C. and C. Stein, A $2\frac{2}{3}$ superstring approximation algorithm (1–3) 29– 57
Bruno, W.J., see E. Knill (1–3) 261–290
DasGupta, B., T. Jiang, S. Kannan, M. Li and E. Sweedyk, On the complexity and approximation of syntenic distance (1–3) 59– 82
Edelsbrunner, H., M. Facello and J. Liang, On the definition and the construction of pockets in macromolecules (1–3) 83–102
Eulenstein, O. and M. Vingron, On the equivalence of two tree mapping measures (1–3) 103–128
Facello, M., see H. Edelsbrunner (1–3) 83–102
Fernández-Baca, D. and J. Lagergren, On the approximability of the Steiner tree problem in phylogeny (1–3) 129–145
Grebinski, V. and G. Kucherov, Reconstructing a Hamiltonian cycle by querying the graph: Application to DNA physical mapping (1–3) 147–165
Gusfield, D., see J. Kececioglu (1–3) 239–260
Gusfield, D., R. Karp, L. Wang and P. Stelling, Graph traversals, genes and matroids: an efficient case of the travelling salesman problem (1–3) 167–180
Heath, L.S. and J.P.C. Vergara, Sorting by bounded block-moves (1–3) 181–206
Hendy, M.D., see M. Steel (1–3) 367–398
Hofacker, I.L., P. Schuster and P.F. Stadler, Combinatorics of RNA secondary structures (1–3) 207–237
Jiang, T., see B. DasGupta (1–3) 59– 82
Kannan, S., see B. DasGupta(1–3) 59– 82
Karp, R., see D. Gusfield (1–3) 167–180
Kececioglu, J.D., see R. Ravi (1–3) 355–368
Kececioglu, J. and D. Gusfield, Reconstructing a history of recombinations from a set of sequences (1–3) 239–260
Knill, E., W.J. Bruno and D.C. Torney, Non-adaptive group testing in the presence of errors (1–3) 261–290
Kucherov, G., see V. Grebinski (1–3) 147–165
Lagergren. J., see Fernández-Baca (1–3) 129–145
Lancia, G. and M. Perlin, Genotyping of pooled microsatellite markers by combinatorial optimization techniques (1–3) 291–314
Li, M., see B. DasGupta (1–3) 59– 82
Liang, J., see H. Edelsbrunner (1–3) 83–102
McMorris, F.R., C. Wang and P. Zhang, On probe interval graphs (1–3) 315–324
Meidanis, J., O. Porto and G.P. Telles, On the consecutive ones property (1–3) 325–354
Penny, D., see M. Steel (1–3) 367–398
Perlin, M., see G. Lancia (1–3) 291–314

Elsevier Science B.V.

Porto, O., see J. Meidanis (1–3) 325–354
Ravi, R. and J.D. Kececioglu, Approximation algorithms for multiple sequence alignment under a fixed evolutionary tree (1–3) 355–368
Schuster, P., see I.L. Hofacker (1–3) 207–237
Stadler, P.F., see I.L. Hofacker (1–3) 207–237
Steel, M., M.D. Hendy and D. Penny, Reconstructing phylogenies from nucleotide pattern probabilities: A survey and some new results (1–3) 367–398
Stein, C., see C. Armen (1–3) 29– 57
Stelling, P., see D. Gusfield (1–3) 167–180
Swaminathan, R., see F. Annexstein (1–3) 7– 28
Sweedyk, E., see B. DasGupta (1–3) 59– 82
Telles, G.P., see J. Meidanis (1–3) 325–354
Torney, D.C., see E. Knill (1–3) 261–290
Vergara, J.P.C., see L.S. Heath (1–3) 181–206
Vingron, M., see O. Eulenstein (1–3) 103–128
Wang, C., see F.R. McMorris (1–3) 315–324
Wang, L., see D. Gusfield (1–3) 167–180
Zhang, P., see F.R. McMorris (1–3) 315–324